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Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Jan Delaval
 Reference Librarian
 Biotechnology & Chemical Library
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 jan.delaval@uspto.gov

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| Date Searcher Picked Up: _____ | Bibliographic _____ | Dr.Link _____ |
| Date Completed: _____ | Litigation _____ | Lexis/Nexis _____ |
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| Online Time _____ | Other _____ | Other (specify) _____ |

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GenScore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

CM nucleotide - nucleotide search, using sw model

Run on: July 9, 2002, 21:41:19 : Search time 1977.29 seconds

(without alignments)
10600.992 Million cell updates/sec

Title: US-09-816-697-1

Feature score: 951
Sequence: 1 atgcacaaatccaaagacaccc.....tgcacaaatccaaagacaccc

Sorted table: IDENTITY_NTC

Gapop 10.0, Gapext 1.0

Scored: 1797656 seqs, 1645628294 residues

Total number of hits satisfying chosen parameters: 675412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post processed: Minimum Match 0%

Maximum Match 100%

Listed first 45 summaries

Database:

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2: gb_bac:
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4: gb_bac:
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33: gb_bac:

Prod. No. is the number of results predicted by chosen to have a score greater than or equal to the score of the result printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match Length DB ID To seq length

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| 2 | 949.4 | 99.8 | 1415 | 6 | AX259777 | AX259777 | Sequence | 1 | from Patent: WO/0173028. | DNA | linear | PAF 26-07-2001 |
| 3 | 670 | 70.5 | 8135 | 6 | AX259779 | AX259779 | Sequence | 1 | from Patent: WO/0173028. | DNA | linear | PAF 26-07-2001 |
| 4 | 670 | 70.5 | 163419 | 9 | HSX04140 | HSX04140 | Sequence | 1 | from Patent: WO/0173028. | DNA | linear | PAF 26-07-2001 |
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| 9 | 159.8 | 16.8 | 1600 | 9 | HSX04140 | HSX04140 | Sequence | 1 | from Patent: WO/0173028. | DNA | linear | PAF 26-07-2001 |
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| 12 | 135.8 | 14.3 | 86080 | 9 | HSX04140 | HSX04140 | Sequence | 1 | from Patent: WO/0173028. | DNA | linear | PAF 26-07-2001 |
| 13 | 134.2 | 14.1 | 181479 | 9 | AC067747 | AC067747 | Sequence | 1 | from Patent: WO/0173028. | DNA | linear | PAF 26-07-2001 |
| 14 | 120.8 | 12.7 | 172485 | 2 | AL591127 | AL591127 | Sequence | 1 | from Patent: WO/0173028. | DNA | linear | PAF 26-07-2001 |
| 15 | 120.8 | 12.7 | 257596 | 2 | AC093448 | AC093448 | Sequence | 1 | from Patent: WO/0173028. | DNA | linear | PAF 26-07-2001 |
| 16 | 118.6 | 12.5 | 137664 | 2 | AC105815 | AC105815 | Sequence | 1 | from Patent: WO/0173028. | DNA | linear | PAF 26-07-2001 |
| 17 | 69.4 | 7.4 | 154746 | 14 | HSV28552 | HSV28552 | Sequence | 1 | from Patent: WO/0173028. | DNA | linear | PAF 26-07-2001 |
| 18 | 69.2 | 7.4 | 199050 | 1 | AC060077 | AC060077 | Sequence | 1 | from Patent: WO/0173028. | DNA | linear | PAF 26-07-2001 |
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| 32 | 60 | 6.3 | 65434 | 2 | AC060610 | AC060610 | Sequence | 1 | from Patent: WO/0173028. | DNA | linear | PAF 26-07-2001 |
| 33 | 60 | 6.3 | 131983 | 8 | AF023240 | AF023240 | Sequence | 1 | from Patent: WO/0173028. | DNA | linear | PAF 26-07-2001 |
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| 35 | 59.8 | 6.3 | 3367 | 6 | AA5258 | AA5258 | Sequence | 1 | from Patent: WO/0173028. | DNA | linear | PAF 26-07-2001 |
| 36 | 59.8 | 6.3 | 43632 | 1 | SC6A5 | SC6A5 | Sequence | 1 | from Patent: WO/0173028. | DNA | linear | PAF 26-07-2001 |
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| 45 | 58.6 | 6.2 | 154180 | 2 | AP004683 | AP004683 | Sequence | 1 | from Patent: WO/0173028. | DNA | linear | PAF 26-07-2001 |

ALIGNMENTS

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| RESULT | 1 | AX259747 | 951 bp | DNA | linear | PAF 26-07-2001 |
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| DEFINITION | AX259747 | Sequence | 1 | from Patent: WO/0173028. | | |
| ACCESSION | AX259747 | GI:16508826 | | | | |
| VERSION | AX259747.1 | | | | | |
| KEYWORDS | human | | | | | |
| SOURCE | human | | | | | |
| ORGANISM | human | | | | | |
| REFERENCE | 1 (str) | | | | | |
| AUTHORS | Lancu, M., Krik, K., Welch, N. and Shaw, J. D. | | | | | |
| TITLE | A p-selectin oligonucleotide ligand (psol) binding protein and uses thereof | | | | | |
| JOURNAL | Patent: WO/0173028 A1 (4-07-2001) | | | | | |
| FEATURES | GENETICS INSTITUTE, INC. (US) | | | | | |
| SOURCE | location/qualifiers | | | | | |
| 1..951 | | | | | | |

Feature: "Human protein product"

[illegible]

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| Fast Local Similarity | 100.08; | Prod. No. 1.26-75; | | |
| Matches 670; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |

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3. CONCLUSION.

Ak018632 1437 bp mRNA linear HTC 19-JAN-2001
Mus musculus adult male Cecum cDNA. RIKEN full-length enriched library; clone:913001Jc17.px domain containing protein, full insert sequence.

Ak018632 61112658437
AK018632.1 G1112658437
HTC: CAP Traport.
Mus musculus (strain:C57BL/6J) adult male Cecum cDNA to mRNA, clone:RIKEN full length enriched mouse cDNA library
clone:913001Zc17.
Mus musculus
Eukaryotic Metazoa: Chordata: Cranialia: Vertebrata: Euteleostomi:
Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.
1 (sites)
Garnier,J.P., and Huchard-Zalc,A.Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 404, 19-44 (1999)

91279254
91279254
103349636
2 (sites)
Garnier,J.P., Shibata,Y., Hayashi,N., Sugahara,Y., Shibata,K.,
Uchi,M., Kato,H., Kawai,T., Meguro,S.M., and Huchard-Zalc,A.Y.
Normalization and subtraction of cap-trapper selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10(12), 1617-1630 (2000)

20439374
11042159
3 (sites)
Shibata,K., Uchi,M., Aizawa,K., Nishikawa,T., Iwasaki,N., Garnier,J.P.,
Kato,H., Aizawa,T., Wada,E., Hayashi,N., Ishihara,H., Uchi,M.,
Saito,N., Ishii,Y., Nakamura,S., Hatama,M., Nishio,K., Harada,A.,
Fujimori,T., Mori,M., Uchi,S., Sakai,H., Kato,H., Ohnishi,K., Takasugi,K.,
Ishikawa,K., Iwawaki,Y., Izumi,M., Ohtani,K., Watabiki,M.,
Yoneda,Y., Ishikawa,T., Oyama,K., Tanaka,I., Matsuyama,S., Kawachi,
H., Uchi,Y., Morikawa,M., Kato,Y., Fuka,A., and Huchard-Zalc,A.Y.
RIKEN integrated sequence analysis (RISA) system -404-format
sequence that pipeline with 484 multiplexed sequencing
coverage from 411, 1737-1771 (2000)

LOCUS AM134842 567 bp mRNA linear EST 28-OCT-1998
DEFINITION GI:11811-383-2-08-0-011 st NCLC/CAP. S833 Homo sapiens cDNA clone
IMAGE:2713048.3', mRNA sequence.
ACCESSION AM134842
VERSION AM134842.1 GI:6138388
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eulimaria; Primates; Carnivora; Hominoidea; Homo.
1 (bases 1 to 567)
MIM:147644
NCBI Gene ID: 2713048
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: capost@ncl.nih.gov
Oligo-dT track not found. Not a site shown in beginning of sequence
is likely internal to the message. cDNA library preparation: M.P.
Stores Lab Clome distribution: M1-CGAP clone distribution
Information can be found through the I.M.A.C.E. Consortium/MLIB at
www.flinch.gov/ncic/cgimr/cgimr.html
Seq primer: M13 Forward
POLYA-Bo: 3'

| FEATURES | LOCAL 100/QUALITY 100 |
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SOURCE
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/lab_host="NCL_COAP_Sub3"
/clone="IMAGE:2713048"
/notes="Vaccinia P7173-Psc (pharmacia)"
/polylinker="Site 1: Not in Site 2: Pro Kit: The NCL_COAP_Sub3 library is a subtracted library derived from the NCL_COAP_Sub1 library, which is a subtracted library derived from R1 at constitutive a mixture of 2:1 normalized or subtracted NCL_COAP libraries: NCL_COAP_S04, NCL_COAP_P22, NCL_COAP_P32, NCL_COAP_S010, NCL_COAP_S015, NCL_COAP_Kid5, NCL_COAP_Kid12, NCL_COAP_Kid3, NCL_COAP_P111, NCL_COAP_P002, NCL_COAP_S022, NCL_COAP_S08, NCL_COAP_S111, NCL_COAP_S024, NCL_COAP_S023, NCL_COAP_S05, NCL_COAP_S076, NCL_COAP_S025. These 21 libraries were pooled and a single-stranded DNA preparation of the resulting mixture was used as a tracer in a subtraction hybridization with a driver whose composition is detailed below: NCL_COAP_Kid3 pool 1 11AM 134 137, 422, 423, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 848, 849, 850, 851, 852, 853, 854, 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872, 873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 885, 886, 887, 888, 889, 890, 891, 892, 893, 894, 895, 896, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910, 911, 912, 913, 914, 915, 916, 917, 918, 919, 920, 921, 922, 923, 924, 925, 926, 927, 928, 929, 930, 931, 932, 933, 934, 935, 936, 937, 938, 939, 940, 941, 942, 943, 944, 945, 946, 947, 948, 949, 950, 951, 952, 953, 954, 955, 956, 957, 958, 959, 960, 961, 962, 963, 964, 965, 966, 967, 968, 969, 970, 971, 972, 973, 974, 975, 976, 977, 978, 979, 980, 981, 982, 983, 984, 985, 986, 987, 988, 989, 990, 991, 992, 993, 994, 995, 996, 997, 998, 999, 1000, 1001, 1002, 1003, 1004, 1005, 1006, 1007, 1008, 1009, 1010, 1011, 1012, 1013, 1014, 1015, 1016, 1017, 1018, 1019, 1020, 1021, 1022, 1023, 1024, 1025, 1026, 1027, 1028, 1029, 1030, 1031, 1032, 1033, 1034, 1035, 1036, 1037, 1038, 1039, 1040, 1041, 1042, 1043, 1044, 1045, 1046, 1047, 1048, 1049, 1050, 1051, 1052, 1053, 1054, 1055, 1056, 1057, 1058, 1059, 1060, 1061, 1062, 1063, 1064, 1065, 1066, 1067, 1068, 1069, 1070, 1071, 1072, 1073, 1074, 1075, 1076, 1077, 1078, 1079, 1080, 1081, 1082, 1083, 1084, 1085, 1086, 1087, 1088, 1089, 1090, 1091, 1092, 1093, 1094, 1095, 1096, 1097, 1098, 1099, 1100, 1101, 1102, 1103, 1104, 1105, 1106, 1107, 1108, 1109, 1110, 1111, 1112, 1113, 1114, 1115, 1116, 1117, 1118, 1119, 1120, 1121, 1122, 1123, 1124, 1125, 1126, 1127, 1128, 1129, 1130, 1131, 1132, 1133, 1134, 1135, 1136, 1137, 1138, 1139, 1140, 1141, 1142, 1143, 1144, 1145, 1146, 1147, 1148, 1149, 1150, 1151, 1152, 1153, 1154, 1155, 1156, 1157, 1158, 1159, 1160, 1161, 1162, 1163, 1164, 1165, 1166, 1167, 1168, 1169, 1170, 1171, 1172, 1173, 1174, 1175, 1176, 1177, 1178, 1179, 1180, 1181, 1182, 1183, 11
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|-----------------------|--------|--------------------|-------|-------------|
| Query Match | 59.58; | Score 565.4; | DH 9; | Length 5677 |
| Best Local Similarity | 99.88; | Pred. No. 3.6e-84; | | |

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[illegible]

Unpublished (1997)
Contact: Robert St

mRNA Sequence

VERSION: 81409524.1 01:15170446

RESEARCH

2000

1. Kujawa et al.

mRNA sequence: [H1439524](#)
[H1439524.1](#) [ct:15170446](#)
 RPT.
 house mouse.
 Mus musculus.
 Eukaryota; Metazoa; Chordata; Vertebrata; Eupoliovirata;

STEFAN, T.

1. *Chlorophyll a* (Chl *a*)

1111 E.
10111111

JOHN R. ...
COMM-FIN

CONTENTS

CONTACT: ROBERT STANSBERG, Ph.D.
Email: rquahrs-r@mail.nih.gov
ISSUE: Environment - Gilbert Smith, Ph.D.



[illegible][illegible]

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|----------|--|--|
| RESULT | 6 | |
| AAK61789 | | |
| TO | AAK61789 standard; cDNA, 588 bp. | |
| XX | | |
| AV | AAK61789; | |
| XX | | |
| 11 | 06 NOV 2001 (first entry) | |
| XX | | |
| 10 | Human immunoglobulin epsilon chain, epsilon 1, cDNA, 588 bp. | |
| XX | | |
| FM | Human; Immunoglobulin epsilon 1, cDNA, 588 bp. | |
| KM | cytotoxic T cell; gene therapy; nucleotide sequence. | |
| XX | | |
| 03 | Human sequences. | |
| XX | | |
| 1N | W0200151182 A2. | |
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| 10 | 09 AUG 2001. | |
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| 17 | JAN 2001; 2001two US01 534. | |
| XX | | |
| 14 | JAN 2000; 2000US 0179065. | |
| 16 | FEB 2000; 2000US 0180628. | |
| 16 | FEB 2000; 2000US 0184664. | |
| 16 | MAY 2000; 2000US 0186450. | |
| 16 | MAY 2000; 2000US 0189874. | |
| 17 | MAY 2000; 2000US 0190076. | |
| 18 | APR 2000; 2000US 0198124. | |
| 18 | MAY 2000; 2000US 0205514. | |
| 19 | JUN 2000; 2000US 0209467. | |
| 19 | JUN 2000; 2000US 0214886. | |
| 20 | JUN 2000; 2000US 0215143. | |
| 07 | JUL 2000; 2000US 0216647. | |
| 07 | JUL 2000; 2000US 0216880. | |
| 11 | JUL 2000; 2000US 0217487. | |
| 14 | JUL 2000; 2000US 0217496. | |
| 14 | JUL 2000; 2000US 0218290. | |

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| 1 | 01 | 07 | N-W-2001 (first entry) | |
| 2 | 02 | 08 | AA228556 | |
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| 5 | 05 | 11 | AA228556 | |
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Genome version 4.5
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3M protein - protein search, using sw model

Run on: July 9, 2002, 15:44:19, Search time 17.41 seconds

(without alignments)
1741.066 Million cell updates/sec

Letter: US-09-816-697-2

Percent score: 16.50

Sequence: 1 MAFEPHPSDGMPTDCT.....KEDPRLDILKELVREYH 816

Scoring table: HUSUM62

Gapop 10.0, Gapext 0.5

Searched: 284139 seqs, 96089324 residues

Total number of hits satisfying chosen parameters: 284138

Minimum hit seq length: 0

Maximum hit seq length: 2000000000

Post-processed: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR_71**

1: p1r1**

2: p1r2**

3: p1r3**

4: p1r4**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 117 | 7.1 | 952 | 2 E84534 | hypothetical prote |
| 2 | 116 | 7.0 | 1010 | 2 T41077 | hypothetical struc |
| 3 | 111 | 6.7 | 473 | 2 T50420 | non-hydrophobic |
| 4 | 111 | 6.7 | 1104 | 2 T40735 | cytochrome c |
| 5 | 111 | 6.7 | 2477 | 1 S020A | specific alpha cha |
| 6 | 102.5 | 6.2 | 1107 | 2 T40735 | specific alpha cha |
| 7 | 102 | 6.2 | 1040 | 2 A42612 | specific alpha cha |
| 8 | 101 | 6.1 | 1425 | 2 T14700 | hypothetical prote |
| 9 | 99.5 | 6.0 | 705 | 2 A45363 | hypothetical prote |
| 10 | 99 | 6.0 | 475 | 2 A07671 | hypothetical prote |
| 11 | 99 | 6.0 | 2472 | 2 A45715 | hypothetical prote |
| 12 | 98 | 5.9 | 456 | 2 T40735 | specific alpha cha |
| 13 | 97.5 | 5.9 | 420 | 2 T08691 | hypothetical prote |
| 14 | 97 | 5.9 | 4664 | 2 A59404 | hypothetical prote |
| 15 | 96 | 5.8 | 441 | 2 T84318 | hypothetical prote |
| 16 | 96 | 5.8 | 4574 | 2 G02520 | conserved hypotet |
| 17 | 95.5 | 5.8 | 473 | 2 T82516 | hypothetical prote |
| 18 | 95.5 | 5.8 | 408 | 2 S75202 | hypothetical prote |
| 19 | 95.5 | 5.8 | 580 | 2 T40735 | specific alpha cha |
| 20 | 95.5 | 5.8 | 411 | 2 A07671 | hypothetical prote |
| 21 | 94.5 | 5.7 | 1082 | 2 H81982 | hypothetical prote |
| 22 | 94.5 | 5.7 | 578 | 2 T21445 | hypothetical prote |
| 23 | 94 | 5.6 | 401 | 2 T43046 | hypothetical prote |
| 24 | 94 | 5.6 | 475 | 2 H27671 | hypothetical prote |
| 25 | 93 | 5.6 | 1466 | 2 T45485 | hypothetical prote |
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| 27 | 92 | 5.6 | 706 | 2 T41077 | hypothetical prote |
| 28 | 92 | 5.6 | 706 | 2 T41077 | hypothetical prote |
| 29 | 92 | 5.6 | 1043 | 2 T42701 | hypothetical prote |

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| 31 | 91 | 5.5 | 448 | 2 D76197 | hypothetical prote |
| 32 | 91 | 5.5 | 640 | 2 S67656 | hypothetical prote |
| 33 | 91 | 5.5 | 892 | 2 T29420 | hypothetical prote |
| 34 | 90.5 | 5.5 | 143 | 2 T40731 | hypothetical prote |
| 35 | 90.5 | 5.5 | 297 | 2 H76706 | hypothetical prote |
| 36 | 90.5 | 5.5 | 472 | 2 D76706 | hypothetical prote |
| 37 | 90.5 | 5.5 | 533 | 2 T76584 | hypothetical prote |
| 38 | 90.5 | 5.5 | 545 | 2 K70374 | hypothetical prote |
| 39 | 90 | 5.5 | 1446 | 1 A45444 | hypothetical prote |
| 40 | 90 | 5.5 | 1460 | 1 E0861F | hypothetical prote |
| 41 | 89.5 | 5.4 | 455 | 2 S15112 | hypothetical prote |
| 42 | 89 | 5.4 | 1162 | 2 D84454 | hypothetical prote |
| 43 | 89 | 5.4 | 4587 | 1 A06638 | hypothetical prote |
| 44 | 88.5 | 5.4 | 950 | 2 F06286 | hypothetical prote |
| 45 | 88.5 | 5.4 | 2591 | 2 T40288 | hypothetical prote |

ALIGNMENTS

RESULT 1

E84534 Hypothetical protein At2g15900 (imported) - Arabidopsis thaliana

CSpecies: Arabidopsis thaliana (mouse-ear cress)

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CSpecies: Arabidopsis thaliana (mouse-ear cress)

Accession references: EMBL:U00957; PIR:FA84876.1; GSPDB:GSPDB01; SRS:SRS016A11.04
 A:Expectimetal source: strain 972b; cosmid cDNA11

Accession: GSPDB:GSPDB016A11.04
 A:Map position: 4

Query Match: 7.00; Score 116; DB 2; Length 1104

Best Local Similarity: 47.48; Pred. No. 0.42; Mismatches 6; Indels 18; Gaps 7

Matches 47; Conservative 47; Mismatches 6; Indels 18; Gaps 7

Accession: GSPDB:GSPDB016A11.04

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Accession: GSPDB:GSPDB016A11.04

Accession references: EMBL:U00957; PIR:FA84876.1; GSPDB:GSPDB01; SRS:SRS016A11.04
 A:Expectimetal source: strain 972b; cosmid cDNA11

Accession: GSPDB:GSPDB016A11.04
 A:Map position: 4

Query Match: 7.00; Score 116; DB 2; Length 1104

Best Local Similarity: 47.48; Pred. No. 0.42; Mismatches 6; Indels 18; Gaps 7

Matches 47; Conservative 47; Mismatches 6; Indels 18; Gaps 7

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Resubmitted to the EMBL Data Library, September 1999

Accession number: Z11608

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Query Match 5.8% Score 96: 10 2: Length 111:
 Best Local Similarity 21.4%: Prod. No. 4.7:
 Matches 90: Conserved 47: Mismatches 132: Indels 114: Gaps 16:

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QY 40 IADHDHETSSSTPEELAYWQLN  YKREVENLEFLAAYGAAVAVVY 96
   | | | | | | | | | | | | | | | | | | | | | | | |
Db 72 IAHFETSAVLSG---VETLGAVVAAGUAGYGGTLLVYV VHDNKGQALITY 127

QY 97 ----QIVV----QIGSHIRKAVLE  KSTIAALGKAL 127
   | | | | | | | | | | | | | | | | | | | | | | | |
Db 128 VHEGTLIFGATLENNSTLNALSKAVYVKKSTLALSKLVPAIMN KTKREKT 187

QY 129 -----KTPRETHVPPPEKHLGNFAHRTVPOOR-----A 160
   | | | | | | | | | | | | | | | | | | | | | | | |
Db 186 KLPRESFVLLAAARWGGKLLMLENAALLAKNSRTRELLGNLLITRRRTGQFA 217

QY 161 LQFYDLIAVIRVRRSK-----EFLD-----PLTRPELR  EAPNATRAVYF 202
   | | | | | | | | | | | | | | | | | | | | | | | |
Db 219 FVGLTFAMH FSVGLSDGAAIYWFAPKLLNGGLYAFVAVVWASTVYV 201P 301

QY 203 KALELLIRLPQEKLTARCPAAVPAALCAVLLCHRDLPRAFAVAPHPALGRLAKES 262
   | | | | | | | | | | | | | | | | | | | | | | | |
Db 302 PAIGCTI SAMPVPEPLQSPEDLAVAQAIYVLAARSSNAVYSAINANMVAINGSKR 360

QY 263 HRYVAP--LIDAVVR-----AVAIQKDFVTLQEPILTESLRRTPR 302
   | | | | | | | | | | | | | | | | | | | | | | | |
Db 361 ---VYHLEKRAETELKREGLNYHEEVAKHETIAVAAHGV FTRGLTFPTVLLVTP 414

QY 393 GILLKELIVREYL 415
   | | | | | | | | | | | | | | | | | | | | | | | |
Db 415 GLEIKIRIKLEHL 427

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Search completed: July 9, 2002, 15:47:20
 Job Name: 151 Seq



| Year | Population | Area | Population | Area |
|------|------------|-------|------------|-------|
| 1970 | 1,275 | 1,275 | 1,275 | 1,275 |
| 1971 | 1,275 | 1,275 | 1,275 | 1,275 |
| 1972 | 1,275 | 1,275 | 1,275 | 1,275 |
| 1973 | 1,275 | 1,275 | 1,275 | 1,275 |
| 1974 | 1,275 | 1,275 | 1,275 | 1,275 |
| 1975 | 1,275 | 1,275 | 1,275 | 1,275 |
| 1976 | 1,275 | 1,275 | 1,275 | 1,275 |
| 1977 | 1,275 | 1,275 | 1,275 | 1,275 |
| 1978 | 1,275 | 1,275 | 1,275 | 1,275 |
| 1979 | 1,275 | 1,275 | 1,275 | 1,275 |
| 1980 | 1,275 | 1,275 | 1,275 | 1,275 |
| 1981 | 1,275 | 1,275 | 1,275 | 1,275 |
| 1982 | 1,275 | 1,275 | 1,275 | 1,275 |
| 1983 | 1,275 | 1,275 | 1,275 | 1,275 |
| 1984 | 1,275 | 1,275 | 1,275 | 1,275 |
| 1985 | 1,275 | 1,275 | 1,275 | 1,275 |
| 1986 | 1,275 | 1,275 | 1,275 | 1,275 |
| 1987 | 1,275 | 1,275 | 1,275 | 1,275 |
| 1988 | 1,275 | 1,275 | 1,275 | 1,275 |
| 1989 | 1,275 | 1,275 | 1,275 | 1,275 |
| 1990 | 1,275 | 1,275 | 1,275 | 1,275 |
| 1991 | 1,275 | 1,275 | 1,275 | 1,275 |
| 1992 | 1,275 | 1,275 | 1,275 | 1,275 |
| 1993 | 1,275 | 1,275 | 1,275 | 1,275 |
| 1994 | 1,275 | 1,275 | 1,275 | 1,275 |
| 1995 | 1,275 | 1,275 | 1,275 | 1,275 |
| 1996 | 1,275 | 1,275 | 1,275 | 1,275 |
| 1997 | 1,275 | 1,275 | 1,275 | 1,275 |
| 1998 | 1,275 | 1,275 | 1,275 | 1,275 |
| 1999 | 1,275 | 1,275 | 1,275 | 1,275 |
| 2000 | 1,275 | 1,275 | 1,275 | 1,275 |
| 2001 | 1,275 | 1,275 | 1,275 | 1,275 |
| 2002 | 1,275 | 1,275 | 1,275 | 1,275 |
| 2003 | 1,275 | 1,275 | 1,275 | 1,275 |
| 2004 | 1,275 | 1,275 | 1,275 | 1,275 |
| 2005 | 1,275 | 1,275 | 1,275 | 1,275 |
| 2006 | 1,275 | 1,275 | 1,275 | 1,275 |
| 2007 | 1,275 | 1,275 | 1,275 | 1,275 |
| 2008 | 1,275 | 1,275 | 1,275 | 1,275 |
| 2009 | 1,275 | 1,275 | 1,275 | 1,275 |
| 2010 | 1,275 | 1,275 | 1,275 | 1,275 |
| 2011 | 1,275 | 1,275 | 1,275 | 1,275 |
| 2012 | 1,275 | 1,275 | 1,275 | 1,275 |
| 2013 | 1,275 | 1,275 | 1,275 | 1,275 |
| 2014 | 1,275 | 1,275 | 1,275 | 1,275 |
| 2015 | 1,275 | 1,275 | 1,275 | 1,275 |
| 2016 | 1,275 | 1,275 | 1,275 | 1,275 |
| 2017 | 1,275 | 1,275 | 1,275 | 1,275 |
| 2018 | 1,275 | 1,275 | 1,275 | 1,275 |
| 2019 | 1,275 | 1,275 | 1,275 | 1,275 |
| 2020 | 1,275 | 1,275 | 1,275 | 1,275 |

Best local similarity

| | | | | |
|-----------------------|-------|------------------|------|----------------|
| Query Match | 7.58 | Score 123 | EB 1 | Length 342 |
| Best Local Similarity | 24.98 | Pred. No. 0.0069 | | |
| Matches | 60 | Conservative | 33 | Mismatches 106 |
| | | | | Indels 42 |
| | | | | Gaps 9 |


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108 EMIL: 026196; AA060464.1;
109 EMIL: A0148008; AA020672.1;
110 RESID: 107741; IABY.
111 MIM: 182810;
112 InterPro: IPR002040; EF hand.
113 InterPro: IPR004542; SH3.
114 InterPro: IPR002017; Spectrin.
115 Pfam: PF00006; cband2.2.
116 Pfam: PF00010; SH3.1.
117 Pfam: PF00455; spectrin.2.
118 Pfam: PF00452; SH3DOMAIN.
119 SMART: SM00004; EFG.2.
120 SMART: SM00426; SH3.1.
121 SMART: SM00150; SPECT.20.
122 PROSITE: PS00010; SPECT.20.
123 PROSITE: PS00002; SH3.1.
124 cytoskeleton. Modulator; Calmodulin binding; Actin binding;
125 cytoplasmic protein; Calcium binding; Repeat; SH3 domain; Polymorphism.
126 REPEAT 10 42 SPECTRIN 1.
127 REPEAT 44 147 SPECTRIN 2.
128 REPEAT 149 453 SPECTRIN 3.
129 REPEAT 255 459 SPECTRIN 4.
130 REPEAT 461 465 SPECTRIN 5.
131 REPEAT 467 571 SPECTRIN 6.
132 REPEAT 573 576 SPECTRIN 7.
133 REPEAT 678 782 SPECTRIN 8.
134 REPEAT 784 888 SPECTRIN 9.
135 REPEAT 890 955 SPECTRIN 10.
136 DOMAIN 967 1026 SH3.
137 REPEAT 1062 1089 SPECTRIN 11.
138 REPEAT 1091 1161 SPECTRIN 12.
139 REPEAT 1208 1251 SPECTRIN 13.
140 REPEAT 1243 1337 SPECTRIN 14.
141 REPEAT 1339 1443 SPECTRIN 15.
142 REPEAT 1445 1549 SPECTRIN 16.
143 REPEAT 1551 1656 SPECTRIN 17.
144 REPEAT 1658 1762 SPECTRIN 18.
145 REPEAT 1764 1868 SPECTRIN 19.
146 REPEAT 1870 1974 SPECTRIN 20.
147 REPEAT 1976 2081 SPECTRIN 21.
148 REPEAT 2091 2195 SPECTRIN 22.
149 REPEAT 2205 2310 SPECTRIN 23.
150 REPEAT 2316 2420 SPECTRIN 24.
151 CA BIND 2426 2447 EF HAND 1 (POTENTIAL).
152 CA BIND 2479 2490 EF HAND 2 (POTENTIAL).
153 CA BIND 1175 1177 FLAVIN (BY MO-CA BIND).
154 VAR1ANT 1400 1400 ZPTID VAR 21.227.
155 CONFLICT 150 150 N - K (IN REF. 2).
156 CONFLICT 498 498 F - S (IN REF. 2).
157 CONFLICT 737 737 V - I (IN REF. 2).
158 CONFLICT 1586 1586 U - Q (SKIT (IN REF. 2)).
159 CONFLICT 1595 1595 F - R (IN REF. 3 AND 4).
160 CONFLICT 1625 1625 N - S (IN REF. 2).
161 CONFLICT 1671 1671 A - P (IN REF. 2).
162 CONFLICT 1918 1918 I - A - D (IN REF. 2).
163 CONFLICT 2447 2448 I - Y (IN REF. 2).
164 CONFLICT 2448 2448 I - Y (IN REF. 2).
165 SUBSEQUENT 2472 AA. 284279 MW. 374196.462A0280. 37644.
166
167 Query Match 6.00% Score 99, 1061, Length 2472.
168 Local Similarity 22.60% Prod. No. 5.5.
169 Matches 69; Conservative 41; Mismatches 141; Indels 54; Gaps 11;

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[illegible]

FT DOMAIN 421 656 D (PRO-RICH LINKER).
 FT DOMAIN 657 706 E.
 FT MOD_RES 9 9 PHOSPHORYLATION (BY GAKR AND
 GAKR KINASE 1).
 FT M_LRES 551 551 PHOSPHORYLATION (BY GAKR).
 FT MOD_RES 568 568 PHOSPHORYLATION (BY GAKR KINASE 11).
 FT MOD_RES 605 605 PHOSPHORYLATION (BY GAKR KINASE 11).
 FT VASGELT 662 673 BR-300000A - KAPPA001 (IN STRAPIN 1B).
 FT VASGELT 671 709 MIST10 (IN STRAPIN 1B).
 SU SEQUENCE 706 AA: 74518 MW: 83476708014340 CROCD

Query Match 5,682 Score 927 DB 17 Length 777
 Host Local Similarity 24,982 Prod. No. 4,52
 Matches 669 Conservative 27 Mismatches 99 Gaps 84 Caps 15

QY 4 PEPTSPGCGKPTTQCTAKTQCEAPATGPDLPHPGPHGLDTHSGSSNMTIKELGG 62
 DB 34 PPAAPSPHATTPATATAPKASSAPAPSPASSSSSSSSSSSSNAVKG11----- 80
 QY 64 YWQNGCFHWYVTVETASAFTEEVYKTVVECTVTCCTPRRA-----VLE 114
 DB 89 -----AAAATFSE-----VGSSTGATMDAAKVLIV10 120
 QY 115 PYSNPAKIQKALEKTFPERF---EIVEEPP---KHLTGFAPEMVTPPKALQFYIA 166
 DB 121 FHTWAWYFKK KKEETELVYDAETSLNVAHAGSEVYGVYKH----- 170
 QY 167 LLYALHGVRRSRRLDF-LTRPELKEAFVCTLRAGYPRALFLLVHLLGKLTARITAA 226
 DB 171 ---GVKVESLEP--DVFIR--GHAFSKANRIR-RSE-----VITIG ----VA 208
 QY 226 AVPALQAVLLCHRDLDKPAFAFAAGKATGRIQANE 261
 DB 209 GHPSTNHLGVYRCKK WYFAQVNLKRLKLTIE 243

Search completed: July 9, 2002, 15:50:41
 Job time: 2.1 sec



[illegible][illegible]

Page 2

| | | | | |
|--------|---|---------------|------|---------|
| RESULT | 6. | | | |
| 014612 | | | | |
| ID | 014612; | PREF:IMINARY: | PRF: | 152 AA. |
| DJ | 01 JAN 1998 (TR EMBL; vol. 05, Created) | | | |
| DJ | 01 JAN 1998 (TR EMBL; vol. 05, last sequence update) | | | |
| DJ | 01 JUN 2001 (TR EMBL; vol. 17, last annotation update) | | | |
| DIC | HYPOHECTICAL 17.8 KDa PROTEIN. | | | |
| COS | Homo sapiens (human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. | | | |
| OX | NBFI TAXID 9606; | | | |
| PN | 11 | | | |
| PT | SOURCE FROM N.A. | | | |
| RX | REEL INFE 97497562; pathmol 9254601; | | | |
| KA | Goto S.-I., Agrawal S.K., Maniokan P., Ohtsumi S.-E., Goto T., Sato | | | |
| KA | Watanabe J.M., Kostor M., Kim Y.S., Emmert Buck M.R., Hotta L.A., | | | |
| KA | Spielvogel A.M., Tomitski M., Roe B.A., Collins F.S., Jordan A.L., | | | |
| KA | Kearse J., et al.; biochemistry 1997; 36(1):1-11. | | | |
| EC | "A transfer map for the 2.8 Mb region containing the multiple | | | |
| PL | restriction site located at 1725-1735 bp (1997)." ; | | | |
| EMBL | EMBL; AF001435; AAA04205.1 ; | | | |
| DG | InterPro: IPR001683; PX. | | | |
| DG | PIfam: PF00787; PX: 1. | | | |
| DJ | SMART: SM00412; PX: 1. | | | |
| KW | Defect loci; Prader-Li. | | | |
| SC | SEQUENCE 152 AA; 1778d MW; 283AAFA6C5A773B8EE CHe004; | | | |

| | | | | | |
|-----------------------|--|-------------------|-------------------|-------------|----------------|
| | Query Match | 7.4% | Score 122; | DH 4; | Length 152; |
| | Host Local Similarity | 27.5%; | Freq. No. 9,0841; | | |
| | Matches | 49; | Conservative | 24; | Mismatches 61; |
| | | | | | Indels 18; |
| | | | | | Gaps 4 |
| <hr/> | | | | | |
| QY | 78 FRASAPFRPKSVVVC ¹¹ VLTSTPANKVALEFVSNAFLSPALRPPREPLED 147 | | | | |
| | : : : : : : : : : : : : : : : : : | | | | |
| DB | 14 YLSQSRPRPE N LARVALA C PEPG VPIVVWVESECTETLTAADMLDLE 72 | | | | |
| QY | 148 VE FRRHSGNANEMTEHEBGALOYEATLTXAYLRKCEDELTLTIDEDENAF 194 | | | | |
| | : : : : : : : : : : : : : : : : : | | | | |
| DB | 74 DEFEATFAAGGVYGRFVASFEREKACGLAEFVHLPALMS | | | | POLKEST 125 |
| QY | 194 GELAKGYPRALPD...LRVP 214 | | | | |
| | : : : : : : : : : : : : : : : : : | | | | |
| DB | 124 KCEVTPLDEVRDLHP 142 | | | | |
| <hr/> | | | | | |
| RESULT | 7 | | | | |
| QYDWEI | | | | | |
| ID | Q9JWE1 | PRELIMINARY: | PRO: | 447 AA. | |
| AC | Q9JWE1 | | | | |
| DT | 01 DEC 2001 (ITEMREL 19, created) | | | | |
| DF | 01 DEC 2001 (ITEMREL 19, last sequence update) | | | | |
| DI | 01 DEC 2001 (ITEMREL 19, last annotation update) | | | | |
| DE | HYPOTHETICAL 47.7 KDa PRETEIN. | | | | |
| OS | Mos musculus (Mouse). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Gracilata; Vertebrata; Euteleostomi; | | | | |
| OT | Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus. | | | | |
| OX | NCBI_TaxID=10390; | | | | |
| RN | 111 | | | | |
| RC | SEQUENCE FROM M.A. | | | | |
| RF | TLSHSE EYE AND RETINA; | | | | |
| RA | SITUATED R ; | | | | |
| KL | Submitted (Oct 2001) to the EMBL/Genbank/DDBJ dat abases. | | | | |
| DR | Unpub. pre016091; AML16091.1 ; | | | | |
| KW | Hydrophobic Protein. | | | | |
| SD | SHOULDNCE 447 AA; 4742 MW; 743924E1BEDDEFAB CFC64; | | | | |
| <hr/> | | | | | |
| Query Match | 7.4%; | Score 122; | DH 11; | Length 447; | |
| Host Local Similarity | 27.5%; | Freq. No. 9,0811; | | | |

| Matches | 309 | Conservative | 24 | Mismatches | 61 | Indels | 18 | gaps | 4 |
|---------|-----|--|-----|------------|----|--------|----|------|---|
| Q7 | 78 | PEIASAALIEKKYKSKVYVQIVIVIGTSGYNKKAVLIEPRTYSNPAKLSKALKTPREEDD | 147 | | | | | | |
| 1b3 | 13 | YTSADPEFHKKGYEKVYVIAQFSKKYVYDIAKEVYKRSYSYDPLKLDLAYTHRNLPK | 72 | | | | | | |
| Q7 | 148 | VE-----PPKRIKGNVALEMLGEPKPAIDGYGLIYALPCYKRSKEDLDLTQPELEAF | 193 | | | | | | |
| 1b1 | 73 | LTETFTATPEAGVYKPKFASVTEKRSKADLDLRTVITFANRIS | 123 | | | | | | |
| Q7 | 194 | GGLKACGYPRALDEL--LKVLP | 213 | | | | | | |
| 1b3 | 124 | ---KGGEVTKPDSYKSKDLKLP | 142 | | | | | | |

| | | |
|---------|--|--------------|
| RESIDUE | 8 | |
| Q9Y343 | | |
| 1D | Q9Y343 | PRELIMINARY; |
| AC | Q9Y343 | PTD; 169 AA. |
| DT | 01-NOV-1999 (TEMBL01, 12, created) | |
| FE | 01-NOV-1999 (TEMBL01, 12, first sequence update) | |
| FT | 01-DEC-2001 (TEMBL01, 19, last annotation update) | |
| FE | HYPOHETICAL 1.8 KDa PROTEIN (SECRETED MIXIN SHH31) PROTEIN). | |
| GN | SHH31 | |
| OS | Homo sapiens (human). | |
| OC | Chordata; Vertebrata; Eumecostomi; | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. | |
| OX | NCBI_TaxID 9606; | |
| RN | 11 | |
| RP | SEQUENCE FROM N.A. | |
| RA | Zhang W., Wan L., Cao X.; | |
| RT | "Hypothetical human protein SHH31." | |
| RE | Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases. | |
| EN | 12 | |
| RP | SEQUENCE FROM N.A. | |
| PA | Hong W.; | |
| RT | "SHH31 as a new member (SHH31) of the sorting nexin family." | |
| FE | Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. | |
| RN | 13 | |
| RP | SEQUENCE FROM N.A. | |
| RT | TISSUE: HUNG CARCINOMA; | |
| RA | Strandberg R.; | |
| FE | Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. | |
| OR | EMBL; AF139461; AAI32668.1; | |
| OR | EMBL; AY044655; AAK98769.1; | |
| OR | EMBL; BC010886; AAI0886.1; | |
| OR | InterPro: IPR001683; PX. | |
| OR | Tram: PF00787; PX: 1. | |
| OR | SMART: SM00312; PX: 1. | |
| OR | Hypothetical protein. | |
| SO | SEQUENCE 169 AA; 19818 MW; 6518364493AEFD; CRC64; | |

[illegible]

Wed Jul 10 06:01:48 2002

us-09-816-697-2.rspt

Page 8

1 RESID: 5
 2 US:08 925 922 2
 3 Sequence #: Affiliated: 02/09/92
 4 Report No: 000412
 5
 6 REVEAL INFORMATION:
 7
 8 APPLICANT: Gilly, Gordon M.
 9 APPLICANT: Kardon, Richard G.
 10 APPLICANT: Schuch, Robert L.
 11 FILER OF INVENTION: Gilly, Gordon M.
 12 NUMBER OF INVENTORS: 27
 13 CORRESPONDENT ADDRESS:
 14 ADDRESSEE: Campbell and Flores
 15 STREET: 4470 La Jolla Village Drive, Suite 700
 16 CITY: San Diego
 17 STATE: California
 18 COUNTRY: USA
 19
 20 ZIP: 92122
 21
 22 COMPUTER READABLE FORM:
 23 MEDIUM TYPE: Floppy disk
 24 COMPUTER: IBM pc compatible
 25 OPERATING SYSTEM: PC DOS/MS-DOS
 26 SOFTWARE: Patcon II Release #1.0, Version #1.25
 27
 28 CURRENT APPLICATION DATA:
 29 APPLICATION NUMBER: 02/09/92
 30 FILING DATE: 01 APR-1992

1 RESUME 4
 2 US-08-890 719-12
 3 Sequence 12, Application US/0889071A
 4 Patent No. 6075129
 5 GENERAL INFORMATION
 6 APPLICANT: BACON, Larry D
 7 APPLICANT: Hunt, Henry D
 8 APPLICANT: Poltore, David
 9 TITLE OF INVENTION: Production of Antisera Specific to Major
 10 TITLE OF INVENTION: Host-compatible and/or B-cell active anti-
 11 FIELD OF INVENTION: Int. Cl. 1977: C07G 23/00, C07G 23/02, C07G 23/04
 12 CURRENT ADDRESS: 1997-07-09
 13 EARLIER APPLICATION NUMBER: 607921, 605
 14 EARLIER FILING DATE: 1996-07-10
 15 NUMBER OF SEQ ID NOS: 49
 16 SOFTWARE: Patent In Ver. 2.1
 17 SEQ ID NO: 12
 18 LENGTH: 438
 19 TYPE: PRT
 20 ORGANISM: Gallus gallus
 21 US-08-890 719-12

| | | | | |
|-----------------------|--------|-----------------|-------|----------------|
| Query Match | 5.28; | Score 85; | IR 3; | Length 338; |
| Fast Local Similarity | 24.78; | Prod. No. 0.39; | | |
| Matches | 54; | Conservative | 24; | Mismatches 67; |
| | | | | Indels 74; |
| | | | | Gaps 13 |

07 250 APTAAAVIAT/AVIAT/IR ILLIADANA A1 250
 100 240 EPPGCEI/EALE/EALE/EALE I 111 111
 100 240 EPPGCEI/EALE/EALE/EALE I 111 111
 07 250 EPPGCEI/EALE/EALE/EALE I 111 111
 100 250 EPPGCEI/EALE/EALE/EALE I 111 111
 07 250 EPPGCEI/EALE/EALE/EALE I 111 111
 100 250 EPPGCEI/EALE/EALE/EALE I 111 111

RESULT 11
 US OR 622 454 7
 Sequence 7, Application US/08622453

1 Patient No. 6700925
 2 GENERAL INFORMATION:
 3 APPLICANT: Bishop, William R.
 4 APPLICANT: Young, Donald B.
 5 APPLICANT: Young, Yind
 6 APPLICANT: Young, James
 7 TITLE OF INVENTION: A STAT-6000 THREAT, SENSING, AND
 8 TITLE OF INVENTION: SENSING FACTOR FROM MYO-ELECTRIC
 9 NUMBER OF SEQUENCES: 9
 10 CORRESPONDENCE ADDRESS:
 11 ADDRESS: Bishop & Associates, LTD
 12 STREET: 1001 G Street, Silverth 11001
 13 CITY: NW
 14 STATE: Washington DC
 15 COUNTRY: USA
 16 ZIP: 20001
 17 COMPUTER READABLE FORM:
 18 MEDIUM TYPE: Floppy disk
 19 COMPUTER: IBM PC compatible
 20 OPERATING SYSTEM: PC-DOS/MS-DOS
 21 SOFTWARE: Patient in Release #1.0, Version #1.25
 22 CURRENT APPLICATION DATA:
 23 APPLICATION NUMBER: US/08622453
 24 FILING DATE:
 25 CLASSIFICATION: 45
 26 ATTORNEY/AGENT INFORMATION:
 27 NAME: Bishop, Yind
 28 REFERENCE NUMBER: 10090
 29 REFERENCE NUMBER: 10090
 30 TELECOMMUNICATION INFORMATION:
 31 TELEPHONE: 202 508 9400
 32 TELEFAX: 202 508 9400
 33 INFORMATION FOR SEQ 10 NO: 1
 34 SEQUENCE CHARACTERISTICS:
 35 LENGTH: 267 amino acids
 36 TYPE: amino acid
 37 TOPOLOGY: linear
 38 MOLECULE TYPE: protein
 39 HYDROTHERMAL: No
 40 ORIGINAL SOURCE:
 41 ORGANISM: Streptomyces coelicolor
 42 US OR 622 454 7

Query Match 4.98; Score 81; DB 1; Length 287
 Local Similarity 21.28; Prod. No. 0.863
 Matches 62; Conservative 98; Mismatches 108; Indels 100; Gaps 15
 07 4 EPPGCEI/EALE/EALE/EALE I 111 111
 100 240 EPPGCEI/EALE/EALE/EALE I 111 111
 07 250 EPPGCEI/EALE/EALE/EALE I 111 111
 100 250 EPPGCEI/EALE/EALE/EALE I 111 111

07 250 EPPGCEI/EALE/EALE/EALE I 111 111
 100 240 EPPGCEI/EALE/EALE/EALE I 111 111
 07 250 EPPGCEI/EALE/EALE/EALE I 111 111
 100 250 EPPGCEI/EALE/EALE/EALE I 111 111
 07 250 EPPGCEI/EALE/EALE/EALE I 111 111
 100 250 EPPGCEI/EALE/EALE/EALE I 111 111

RESULT 12
 US OR 622 454 7
 Sequence 7, Application US/08622452A

1 Patient No. 682546
 2 GENERAL INFORMATION:
 3 APPLICANT: Bishop, William R.
 4 APPLICANT: Young, James
 5 TITLE OF INVENTION: A STAT-6000 THREAT, SENSING, AND
 6 TITLE OF INVENTION: SENSING FACTOR FROM MYO-ELECTRIC
 7 NUMBER OF SEQUENCES: 11
 8 CORRESPONDENCE ADDRESS:
 9 ADDRESS: Bishop & Associates, LTD
 10 STREET: 1100 New York Avenue, N.W.
 11 CITY: Washington
 12 STATE: DC
 13 COUNTRY: USA
 14 ZIP: 20005-3918
 15 COMPUTER READABLE FORM:
 16 MEDIUM TYPE: Floppy disk
 17 COMPUTER: IBM PC compatible
 18 OPERATING SYSTEM: PC-DOS/MS-DOS
 19 SOFTWARE: Word Perfect
 20 CURRENT APPLICATION DATA:
 21 APPLICATION NUMBER: US/08622452A
 22 FILING DATE: 27 MAR-1996
 23 CLASSIFICATION: 45
 24 INFORMATION FOR SEQ 10 NO: 9
 25 SEQUENCE CHARACTERISTICS:
 26 LENGTH: 287 amino acids
 27 TYPE: amino acid
 28 TOPOLOGY: linear
 29 MOLECULE TYPE: protein
 30 HYDROTHERMAL: No
 31 ORIGINAL SOURCE:
 32 ORGANISM: Streptomyces coelicolor
 33 US OR 622 454 7

Query Match 4.98; Score 81; DB 2; Length 287

Local Similarity 21.28; Prod. No. 0.863
 Matches 62; Conservative 98; Mismatches 108; Indels 100; Gaps 15
 07 4 EPPGCEI/EALE/EALE/EALE I 111 111
 100 240 EPPGCEI/EALE/EALE/EALE I 111 111
 07 250 EPPGCEI/EALE/EALE/EALE I 111 111
 100 250 EPPGCEI/EALE/EALE/EALE I 111 111
 07 250 EPPGCEI/EALE/EALE/EALE I 111 111
 100 250 EPPGCEI/EALE/EALE/EALE I 111 111

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